In the Specification, on page 1, following paragraph 1, insert:

- - BACKGROUND OF THE INVENTION - -.

On page 2, before the second full paragraph insert:

- - SUMMARY OF THE INVENTION - -.

On page 2, before the fourth full paragraph, insert:

- - BRIEF DESCRIPTION OF THE FIGURES - -.

Fig. 1. SDS-PAGE gel electrophoresis and immunoblots of *L. intracellularis* whole cells and *L. intracellularis* outer membrane preparation probed with rabbit antisera. Lanes: 1, Prestained precision markers (BioRad); 2, *L. intracellularis* total cell extract; 3, *L. intracellularis* outer membrane preparation. Panels; A: protein visualization with Coomassie brilliant blue, B: blot probed with serum raised against purified outer membrane proteins (R279); C, blot probed with serum raised against whole cells (R291). The 19/21 kD, 37 kD and 50 kD protein are indicated with P1/P2, P4 and P5 respectively.

Fig. 2. Overexpression of the 50 kD protein. The protein was overexpressed in BL21(DE3) containing various pET24a-derived constructs as described in text. Total cell extracts were separated by SDS-PAGE and either stained with Coomassie brilliant blue (Panel A) or blotted on an Immobilon-P PVDF membrane and probed with antiserum obtained from experimentally infected pigs (Panel B). Lane 1: pre-stained precision marker (BioRad) band of 45 kDa; lane 2: BL21-P5-a; Lane 3: BL21-P5-f; lane 4: purified *L. intracellularis* outer membrane proteins (only 50 kD protein visible). Lane 5: BL21-P5-a uninduced.

On page 3, replace the fifth paragraph with the following:

- -The level of nucleotide homology can be determined with the computer program "BLAST 2 SEQUENCES" by selecting sub-program: "BLASTN." ~~that can be found at www.ncbi.nlm.nih.gov/blast/b12.html.~~

A reference for this program is Tatiana A. Tatusova, Thomas L. Madden FEMS Microbiol. Letters 174: 247-250 (1999). Parameters used are the default parameters:
Reward for a match: +1. Penalty for a mismatch: -2. Open gap: 5. Extension gap: 2. Gap x_dropoff: 50. - -

On page 9, replace the second full paragraph with the following:

- -The level of protein homology can be determined with the computer program "BLAST 2 SEQUENCES" by selecting sub-program: "BLASTP." ~~that can be found at www.ncbi.nlm.nih.gov/blast/b12.html.~~

A reference for this program is Tatiana A. Tatusova, Thomas L. Madden FEMS Microbiol. Letters 174: 247-250 (1999). Matrix used: "blosum62". Parameters used are the default parameters:
Open gap: 11. Extension gap: 1. Gap x_dropoff: 50. - -

On page 12, replace the table with the following:

Peptide 1	Peptide 2	Peptide 3
Forward primers	Forward primers	Forward primer
ggI acI caR gaR taY aaY tt SEQ ID NO: 21	gcI taY gaY taY ttR gtI atg SEQ ID NO: 25	TtY taY gtI atg gtI tgg ac SEQ ID NO: 29
ggI acI caR gaR taY aaY ct SEQ ID NO: 22	gcI taY gaY taY ctI gtI atg SEQ ID NO: 26	
Reverse primers	Reverse primers	Reverse primer
AaR ttR taY tcY tgI gtI cc SEQ ID NO: 23	cat Iac Yaa Rta Rtc Rta Igc SEQ ID NO: 27	Gtc caI acc atI acR taR aa SEQ ID NO: 30
AaR ttR taY tcY tgI gtI cc SEQ ID NO: 24	cat Iac Iag Rta Rtc Rta Igc SEQ ID NO: 28	

On page 25, replace Table 1 with the following:

Table 1. Obtained protein sequences

Protein	Peptide	Sequence	Sequence Id No:
19 kD	Internal	AAYEYLVMLGVN	SEQ ID NO: 5
	Internal	PFYVMVW	SEQ ID NO: 31
	Internal	GTQEYNLALGER	SEQ ID NO: 6
21 kD	Internal	AAYEYLVMLGVN	SEQ ID NO: 5
	Internal	PFYVMVW	SEQ ID NO: 7
	Internal	GTQEYNLALGER	SEQ ID NO: 6
37 kD	N-terminal	AEVTASCTKRVG	SEQ ID NO: 15
	Internal	SDLEIFGR	SEQ ID NO: 32
	Internal	GVNFAFDSFALDDTAK	SEQ ID NO: 16
50 kD	N-terminal	IDFKAKGVWDFN	SEQ ID NO: 17
	Internal	KDYAWEVDFDT	SEQ ID NO: 18

Please cancel page 26 without prejudice or disclaimer.

On page 27, replace "Claims" with - - We claim: - -